

(1) GENERAL INFORMATION:

- (i) APPLICANT: (Countries other than US) AMRAD OPERATIONS PTY LTD
(US only) WILLSON, T; NICOLA, NA; HILTON, DJ;
METCALF, D ZAN, JG
- (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND
GENETIC SEQUENCES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT INTERNATIONAL
(B) FILING DATE: 23-OCT-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PN6135/95
(B) FILING DATE: 23-OCT-1995
(A) APPLICATION NUMBER: PN7276/95
(B) FILING DATE: 22-DEC-1995
(A) APPLICATION NUMBER: PO2208/96
(B) FILING DATE: 09-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: HUGHES DR, E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/EK
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +61 3 9254 2777
(B) TELEFAX: +61 3 9254 2770

090713Z = 060900Z

- 48 -

(1) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: ...1278
- (C) X, unknown nucleotide;
Xaa, unknown amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGAAAAGATA GAATAAATGG CCTCGTGCCG AATTCGGCAC GAGCCGAGGC GAGGGCCTGC -1
 ATG GCG CGG CCA GCG CTG CTG GGC GAG CTG TTG GTG CTG CTA CTG TGG 48
 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1 5 10 15
 ACC GCC ACC GTG XXX GGC CAA GTT GCC GCG GCC ACA GAA GTT CAG CCA 96
 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 20 25 30
 CCT GTG ACG AAT TTG AGC GTC TCT GTC GAA AAT CTC TGC ACG ATA ATA 144
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 35 40 45
 TGG ACG TGG AGT CCT CCT GAA GGA GCC AGT CCA AAT TGC ACT CTC AGA 192
 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 50 55 60
 TAT TTT AGT CAC TTT GAT GAC CAA CAG GAT AAG AAA ATT GCT CCA GAA 240
 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80
 ACT CAT CGT AAA GAG GAA TTA CCC CTG GAT GAG AAA ATC TGT CTG CAG 288
 Thr His Arg Lys Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 85 90 95
 GTG GGC TCT CAG TGT AGT GCC AAT GAA AGT GAG AAG CCT AGC CCT TTG 336
 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 100 105 110
 GTG AAA AAG TGC ATC TCA CCC CCT GAA GGT GAT CCT GAG TCC GCT GTG 384
 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

0051843-062999

- 49 -

ACT GAG CTC AAG TGC ATT TGG CAT AAC CTG AGC TAT ATG AAG TGT TCC	432
Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	
130 135 140	
TGG CTC CCT GGA AGG AAT ACA AGC CCT GAC ACA CAC TAT ACT CTG TAC	480
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr	
145 150 155 160	
TAT TGG TAC AGC AGC CTG GAG AAA AGT CGT CAA TGT GAA AAC ATC TAT	528
Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr	
165 170 175	
AGA GAA GGT CAA CAC ATT GCT TGT TCC TTT AAA TTG ACT AAA GTG GAA	576
Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu	
180 185 190	
CCT XXX AGT TTT GAA CAT CAG AAC GTT CAA ATA ATG GTC AAG GAT AAT	624
Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn	
195 200 205	
GCT GGG AAA ATT AGG CCA TCC TGC AAA ATA GTG TCT TTA ACT TCC TAT	672
Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr	
210 215 220	
GTG AAA CCT GAT CCT CCA CAT ATT AAA CAT CTT CTC CTC AAA AAT GGT	720
Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly	
225 230 235 240	
GCC TTA TTA GTG CAG TGG AAG AAT CCA CAA AAT TTT AGA AGC AGA TGC	768
Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys	
245 250 255	
TTA ACT TAT GAA GTG GAG GTC AAT AAT ACT CAA ACC GAC CGA CAT AAT	816
Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn	
260 265 270	
ATT TTA GAG GTT GAA GAG GAC AAA TGC CAG AAT TCC GAA TCT GAT AGA	864
Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg	
275 280 285	
AAC ATG GAG GGT ACA AGT TGT TTC CAA CTC CCT GGT GTT CTT GCC GAC	912
Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp	
290 295 300	
GCT GTC TAC ACA GTC AGA GTA AGA GTC AAA ACA AAC AAG TTA TGC TTT	960
Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe	
305 310 315 320	
GAT GAC AAC AAA CTG TGG AGT GAT TGG AGT GAA GCA CAG AGT ATA GGT	1008
Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly	
325 330 335	
AAG GAG CAA AAC TCC ACC TTC TAC ACC ACC ATG TTA CTC ACC ATT CCA	1056
Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro	
340 345 350	

066290" 243-062998

- 50 -

GTC TTT GTC GCA GTG GCA GTC ATA ATC CTC CTT TTT TAC CTG AAA AGG 1104
 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 355 360 365

CTT AAG ATC ATT ATA TTT CCT CCA ATT CCT GAT CCT GGC AAG ATT TTT 1152
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

AAA GAA ATG TTT GGA GAC CAG AAT GAT GAT ACC CTG CAC TGG AAG AAG 1200
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400

TAT GAC ATC TAT GAG AAA CAA TCC AAA GAA GAA ACG GAT TCT GTA GTG 1248
 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

CTG ATA GAA AAC CTG AAG AAA GCA GCT CCT TGATGGGGAG AAGTGATTTC 1298
 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
 420 425

TTTCTTGCCT TCAATGTGAC CCTGT 1323

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1 5 10 15

Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 85 90 95

09051843-1062996

- 51 -

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 100 105 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 145 150 155 160

Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 165 170 175

Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 180 185 190

Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 195 200 205

Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
 225 230 235 240

Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 245 250 255

Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 260 265 270

Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 275 280 285

Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 290 295 300

Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 305 310 315 320

Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 325 330 335

Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
 340 345 350

Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 355 360 365

Leu Lys Il Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

00051843.062998

- 52 -

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
 420 425

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGTCTAACA CGGACCAAGG AGTTTAACAC GTGCGGCCGG GTTCCGAGGC GAGAGGCTGC -1

ATG GAG TGG CCG GCG CGG CTC TGC GGG CTG TGG GCG CTG CTG CTC TGC 48
 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15

GCC GGC GGC GGG GGC GGG GGC GGG GGC GCG CCT ACG GAA ACT CAG CCA 96
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 20 25 30

CCT GTG ACA AAT TTG AGT GTC TCT GTT GAA AAC CTC TGC ACA GTA ATA 144
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 35 40 45

TGG ACA TGG AAT CCA CCC GAG GGA GCC AGC TCA AAT TGT AGT CTA TGG 192
 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60

TAT TTT AGT CAT TTT GGC GAC AAA CAA GAT AAG AAA ATA GCT CCG GAA 240
 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

ACT CGT CGT TCA ATA GAA GTA CCC CTG AAT GAG AGG ATT TGT CTG CAA 288
 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
 85 90 95

066290-069990

- 53 -

GTG GGG TCC CAG TGT AGC ACC AAT GAG AGT GAG AAG CCT AGC ATT TTG	336
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu	
100 105 110	
GTT GAA AAA TGC ATC TCA CCC CCA GAA GGT GAT CCT GAG TCT GCT GTG	384
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val	
115 120 125	
ACT GAA CTT CAA TGC ATT TGG CAC AAC CTG AGC TAC ATG AAG TGT TCT	432
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	
130 135 140	
TGG CTC CCT GGA AGG AAT ACC AGT CCC GAC ACT AAC TAT ACT CTC TAC	480
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr	
145 150 155 160	
TAT TGG CAC AGA AGC CTG GAA AAA ATT CAT CAA TGT GAA AAC ATC TTT	528
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe	
165 170 175	
AGA GAA GGC CAA TAC TTT GGT TGT TCC TTT GAT CTG ACC AAA GTG AAG	576
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys	
180 185 190	
GAT TCC AGT TTT GAA CAA CAC AGT GTC CAA ATA ATG GTC AAG GAT AAT	624
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn	
195 200 205	
GCA GGA AAA ATT AAA CCA TCC TTC AAT ATA GTG CCT TTA ACT TCC CGT	672
Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg	
210 215 220	
GTG AAA CCT GAT CCT CCA CAT ATT AAA AAC CTC TCC TTC CAC AAT GAT	720
Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp	
225 230 235 240	
GAC CTA TAT GTG CAA TGG GAG AAT CCA CAG AAT TTT ATT AGC AGA TGC	768
Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys	
245 250 255	
CTA TTT TAT GAA GTA GAA GTC AAT AAC AGC CAA ACT GAG ACA CAT AAT	816
Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn	
260 265 270	
GTT TTC TAC GTC CAA GAG GCT AAA TGT GAG AAT CCA GAA TTT GAG AGA	864
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg	
275 280 285	
AAT GTG GAG AAT ACA TCT TGT TTC ATG GTC CCT GGT GTT CTT CCT GAT	912
Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp	
290 295 300	
ACT TTG AAC ACA GTC AGA ATA AGA GTC AAA ACA AAT AAG TTA TGC TAT	960
Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr	
305 310 315 320	

09051843 060998

- 54 -

GAG GAT GAC AAA CTC TGG AGT AAT TGG AGC CAA GAA ATG AGT ATA GGT 1008
 Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
 325 330 335

AAG AAG CGC AAT TCC ACA CTC TAC ATA ACC ATG TTA CTC ATT GTT CCA 1056
 Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
 340 345 350

GTC ATC GTC GCA GGT GCA ATC ATA GTA CTC CTG CTT TAC CTA AAA AGG 1104
 Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
 355 360 365

CTC AAG ATT ATT ATA TTC CCT CCA ATT CCT GAT CCT GGC AAG ATT TTT 1152
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

AAA GAA ATG TTT GGA GAC CAG AAT GAT GAT ACT CTG CAC TGG AAG AAG 1200
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400

TAC GAC ATC TAT GAG AAG CAA ACC AAG GAG GAA ACC GAC TCT GTA GTG 1248
 Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

CTG ATA GAA AAC CTG AAG AAA GCC TCT CAG TGATGGAGAT AATTTATTTT 1298
 Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

TACCTTCACT GTGACCTTGA GAAGA 1323

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15

Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60

09051843 062998

- 55 -

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys
245 250 255

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

00051843.062998

- 56 -

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
 355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu Leu
 5 10 15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Tyr Lys Asp Asp Asp Asp Lys
 5

09051843-1062998

- 57 -

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCTTCTAGA ACAGAAGTTC AGCCACCTGT G

31

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACTCCACCT TCTACACCAC CTGATCTAGA

30

0905143 E4815060
Sub
cont